



SEQUENCE LISTING

<110> Kato, Seiji
 Kimura, Tomoko
 Saito, Shinji
 Kobayashi, Midori

<120> HUMAN PROTEIN HAVING TRANSMEMBRANE DOMAINS AND cDNAs
 ENCODING THESE PROTEINS

<130> PCT-6711PUS

<150> JP 9/276,171

<160> 1847-10-2

<140> 09/529,205

<161> 22,07-07-21

<160> 49

<170> PatentIn Ver. 2.0

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<212> PRT

<213> Homo sapiens

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Try Thr Ala Arg Ile Arg Ala Val Gly Leu Ile Thr Val Ile Ser Lys
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Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly

Tyr Ile Asn Ile Thr Tyr Tyr Asp Thr Asp Leu Ser Asn Ala Ser Asp

Ala His Ala Leu Ile Pro Ala Ala Ala Ile Leu Ala Ile Ile Pro Ala
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Leu Gly Leu Leu Ile Trp Gly Pro Gly Gln Leu
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Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly
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Thr Leu Gly Thr Ile Val Cys Ala Leu Pro Met Trp Asp Val Ser
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Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Ile Asn Ile Thr Glu Gly
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Leu Trp Met Asn Cys Val Val Glu Ser Thr Gly Gln Met Gln Cys Lys
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Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg
 65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Ala Ala Phe Gly Leu Leu Val
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Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
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Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala
 115 120 125

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
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Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly
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Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala Leu Gln Leu Leu Gly
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Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr
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Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala
 195 200 205

Ser Leu Gly Thr Gly Asp Asp Asp Asp Asp Val Val
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 220-225
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Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Tyr
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Tyr Leu Ile Trp Leu Ile Ala Phe Leu Ala Gln Leu Asn Pro Leu Thr
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Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp
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Pro

• 210 • 4
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 • 212 • PRT
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Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu Arg
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Itp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile Gly
 50 55 60

Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro Ala
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Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly Pro
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Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn Met
 100 105 110

Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu Ile
 115 120 125

Ile Arg Ile Arg Pro Asn Ile Ala Ile Gly Val Pro Ala Ile Asn Arg
 130 135 140

Ile Ile Arg Leu Ile Arg Arg Ile Ile Ala Arg Asn Itp Asn Asn Thr
 145 150 155

Arg Ser Arg Leu Ily Ser Ala Leu Arg Pro Leu Ala Asp Iys Ile Leu
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Ile Val Leu Ile Ile Ile Ile Ile Tyr Ile Asn Arg Leu Ile Ile Ile
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Ile Ser Lys Val Asn Thr Ala Val Glu Leu Ile Leu Val Ala Ala Ser			
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Ile Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Glu Ile			
223	224	225	226
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Gly Asp Lys Ieu Lys Ile Asn Ile Asp Val Ieu Ile Ile His Met Pro
 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

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Val Thr Val Pro Asp Thr Asp Ser Leu Asp Thr Asp Asn Tyr Glu Ser

Asp Thr Ile Glu Glu Cys Arg Arg Glu Gly Phe Ser Glu Lys Met Glu
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160 165 170 175

Lys Val Ala Gly Asn Ile His Phe Ala Ile Gly Lys Ser Ile Glu
180 185 190 195

Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile
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Asn Met Thr His Tyr Ile Glu His Leu Ser Phe Gly Gln Asp Tyr Pro
220 225 230 235

Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Glu Ala
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Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met
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His Glu Lys Val Ala Asn Gly Leu Leu Gly Asp Gln Gly Leu Pro Gly
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Val Phe Val Leu Tyr Glu Leu Ser Pro Met Met Val Lys Leu Thr Glu
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Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile
345 350 355 360

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His
365 370 375 380

Ser Ala Arg Ala Ile Gln Lys Ile Asp Leu Gly Lys Thr Thr
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Met Thr Arg Leu Leu Gly Tyr Val Asp Ile Leu Arg Leu Ser Ile Val
410 415 420 425 430 435 440 445 450

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 Leu Gly Leu Gly Val Val Leu Val Ser Ser Phe Phe Ala Leu Gly
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 Phe Ala Gly Thr Phe Leu Gly Asp Tyr Ile Gly Ile Leu Lys Glu Ala
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 Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro
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 Thr Gly Leu Ile Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala
 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240
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 Ala Leu Asp Leu Leu Gly Val Glu Asp Ala Leu Ala Leu Pro
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128	129	130
Asp Asn Gln Ile Cys Gln Gly Glu Lys Asn Leu Cys Arg Asn Thr Gly	131	132
133	134	135
Asp Pro Gln Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp Gly Pro	136	137
138	139	140
Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Ile His Gly Tyr Lys Cys	141	142
143	144	145
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Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro	39	40
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Ala Arg Ile Thr Ile Glu Pro Thr Ser Glu Leu Ile Ile Ile Lys	43	44
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Thr Asp Ile Ile Ile Val Ile	47	48
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Ala Ala His Pro Thr Asp Asp Thr Thr Ile Leu Ser Ile Arg Pro Ser	51	52
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Pro Thr Thr Asp Val Glu Thr Asp Glu Val Thr Ile Ile Ile Ile Ile Ile	55	56
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Arg Gly Ileu Ileu Val Ala Ala Val Leu Ileu Ileu Thr Gly Ileu Ileu Ileu
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Ileu Thr Ser Gly Lys Cys Arg; Gln Leu Ser Arg; Leu Cys Arg; Asn His
152 153 154 155 156 157 158 159 160 161 162 163

Cys Arg;

Arg 164
Arg 165 166
Arg 167 168
Arg 169 Human sapiens

Arg 170 171
Ser Arg Ileu Thr Arg; Lys Arg; Leu Cys Ser Ileu Leu Ileu Ala Ileu Tyr
171 172 173 174 175 176 177

Cys Ileu Phe Ser Ileu Tyr Ala Ala Tyr His Val Phe Ileu Gly Arg; Arg
178 179 180 181 182 183 184

Arg; Gln Ala Ileu Ala Gly Ser Pro Arg; Gly Ileu Arg; Lys Gly Ala Ala
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Pro Ala Arg; Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu
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Gln Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
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Phe Lys Thr Ser Ileu Gln Ileu Leu Asp Lys Ser Thr Lys Gly Lys Thr
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Asp Ileu Ser Val Gln Ileu Ileu Trp Gly Lys Ala Ala Ileu Gly Ileu Tyr Leu
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Trp Glu His Ileu Phe Glu Gly Ileu Ileu Asp Pro Ser Asp Val Thr Ala
225 226 227 228 229 230 231 232

Gln Thr Arg; Glu Gly Lys Ser Ileu Val Gly Arg; Thr Gln Tyr Ser Ileu
233 234 235 236 237 238 239 240

Asp Ileu Asp Pro Asn Val Ileu Ileu Asp Thr Asp Val Asp Thr Asp
241 242 243 244 245 246 247 248 249 250 251 252

Arg Thr Val Thr Ileu Ileu Tyr Ala Glu Asn Leu Val Gln Thr Glu Lys
253 254 255 256 257 258 259 260 261 262 263 264

Asn Thr Val Thr Ileu Ileu Tyr Ala Glu Asn Leu Val Gln Thr Glu Lys
265 266 267 268 269 270 271 272 273 274 275 276

Ala Thr Val Thr Ileu Ileu Tyr Ala Glu Asn Leu Val Gln Thr Glu Lys
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Ala Ser Trp Ser Met Leu His Asp Glu Arg Ile Tyr Leu Cys Asn Ile	365	370	375	380
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Val Glu Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His	485	490	495	500
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Trp Tyr Gln His Ile Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile	565	570	575	580
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<213> Homo sapiens

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- 211 - 243
- 212 - tRNA
- 213 - Homo sapiens

240

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•212: DNA
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112 *Journal of Health Politics*

2 2 1 1

2011-16
2011-18
2011-19
2011-20
2011-21 Home samples

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400 17

Digitized by srujanika@gmail.com

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1. *18S rRNA*
2. *28S rRNA*
3. *5S rRNA*
4. *16S rRNA*
5. *23S rRNA*

卷之三

634

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430 15

162

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1991-1994
1995-1998
1999-2002

1000

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 Trp Thr Ala Asn Ile Asp Ala Val Gly Ieu Leu Thr Val Ile Ser Lys
 34 44
 Gly Cys Ser Ieu Asn Cys Val Asp Asp Ser Glu Asp Tyr Tyr Val Gly
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Opposition to the proposed legislation was led by the National Farmers' Federation, which argued that the bill would not only increase the cost of production for farmers but also reduce the quality of the food supply.

¹⁰ See, for example, the discussion of the 1992 Constitutional Convention in the *Constitutional Convention of 1992: The People's Assembly* (1993).

446 Asn Cys Val Val Glu Ser Thr Gly Glu Met Glu Pys Lys Val Tyr Asp
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82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 299 300 301 302 303 304 305 306 307 308 309 309 310 311 312 313 314 315 316 317 318 319 319 320 321 322 323 324 325 326 327 328 329 329 330 331 332 333 334 335 336 337 338 339 339 340 341 342 343 344 345 346 347 348 349 349 350 351 352 353 354 355 356 357 358 359 359 360 361 362 363 364 365 366 367 368 369 369 370 371 372 373 374 375 376 377 378 379 379 380 381 382 383 384 385 386 387 388 389 389 390 391 392 393 394 395 396 397 398 399 399 400 401 402 403 404 405 406 407 408 409 409 410 411 412 413 414 415 416 417 418 419 419 420 421 422 423 424 425 426 427 428 429 429 430 431 432 433 434 435 436 437 438 439 439 440 441 442 443 444 445 446 447 448 449 449 450 451 452 453 454 455 456 457 458 459 459 460 461 462 463 464 465 466 467 468 469 469 470 471 472 473 474 475 476 477 478 479 479 480 481 482 483 484 485 486 487 488 489 489 490 491 492 493 494 495 496 497 498 499 499 500 501 502 503 504 505 506 507 508 509 509 510 511 512 513 514 515 516 517 518 519 519 520 521 522 523 524 525 526 527 528 529 529 530 531 532 533 534 535 536 537 538 539 539 540 541 542 543 544 545 546 547 548 549 549 550 551 552 553 554 555 556 557 558 559 559 560 561 562 563 564 565 566 567 568 569 569 570 571 572 573 574 575 576 577 578 579 579 580 581 582 583 584 585 586 587 588 589 589 590 591 592 593 594 595 596 597 598 599 599 600 601 602 603 604 605 606 607 608 609 609 610 611 612 613 614 615 616 617 618 619 619 620 621 622 623 624 625 626 627 628 629 629 630 631 632 633 634 635 636 637 638 639 639 640 641 642 643 644 645 646 647 648 649 649 650 651 652 653 654 655 656 657 658 659 659 660 661 662 663 664 665 666 667 668 669 669 670 671 672 673 674 675 676 677 678 679 679 680 681 682 683 684 685 686 687 688 689 689 690 691 692 693 694 695 696 697 698 699 699 700 701 702 703 704 705 706 707 708 709 709 710 711 712 713 714 715 716 717 718 719 719 720 721 722 723 724 725 726 727 728 729 729 730 731 732 733 734 735 736 737 738 739 739 740 741 742 743 744 745 746 747 748 749 749 750 751 752 753 754 755 756 757 758 759 759 760 761 762 763 764 765 766 767 768 769 769 770 771 772 773 774 775 776 777 778 779 779 780 781 782 783 784 785 786 787 788 789 789 790 791 792 793 794 795 796 797 798 799 799 800 801 802 803 804 805 806 807 808 809 809 810 811 812 813 814 815 816 816 817 818 819 819 820 821 822 823 824 825 826 827 828 829 829 830 831 832 833 834 835 836 837 838 839 839 840 841 842 843 844 845 846 847 848 849 849 850 851 852 853 854 855 856 857 858 859 859 860 861 862 863 864 865 866 867 868 869 869 870 871 872 873 874 875 876 877 878 879 879 880 881 882 883 884 885 886 887 888 889 889 890 891 892 893 894 895 896 897 898 899 899 900 901 902 903 904 905 906 907 908 909 909 910 911 912 913 914 915 916 917 918 919 919 920 921 922 923 924 925 926 927 928 929 929 930 931 932 933 934 935 936 937 938 939 939 940 941 942 943 944 945 946 947 948 949 949 950 951 952 953 954 955 956 957 958 959 959 960 961 962 963 964 965 966 967 968 969 969 970 971 972 973 974 975 976 977 978 979 979 980 981 982 983 984 985 986 987 988 989 989 990 991 992 993 994 995 996 997 998 999 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 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1191 1192 1193 1194 1195 1196 1197 1198 1199 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1549 1550 1551 1552 1553 1554 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2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2319 2320 23

Homo sapiens

1.19

Met 1-24
 Met 1-25
 Met 1-26
 Met 1-27

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Ile
 1 5 10 15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Leu Met Trp Arg Val Thr
 20 25 30

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly
 35 40 45

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys
 50 55 60

Val Tyr Asp Ser Leu Leu Ala Leu Ile Gln Asp Leu Glu Ala Ala Arg
 65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Ile Gly Leu Leu Val
 85 90 95

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala
 100 105 110

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Ile Leu Leu Ala Ala
 115 120 125

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg
 130 135 140

Asp Thr Tyr Asn Pro Val Val Pro Gln Ala Gln Lys Arg Glu Met Gly
 145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Arg Leu Gln Leu Leu Gly
 165 170 175 180

Arg Asn Leu Leu Thr Tyr Ser Gly Ile Asp Arg Lys Arg Ile Asp Ile
 185 190 195 200

Asp Asn Ile Val Val Val Tyr Asp Asn Pro Asp Asp Asp Asp Asp Ile
 205 210 215 220 225 230

Asp Leu Gly Thr Ile Tyr Asp Arg Lys Asp Asp Tyr Val
 235 240 245 250

1993
1993 (EB) .. (1993)

Trp Gly Ile Val Asp Phe Leu Val Pro Trp Phe Ile Pro Gly Ile Pro

Asp³⁵ Arg³⁶ Ile³⁷ Ile³⁸ Thr³⁹ Met⁴⁰ Val⁴¹ Thr⁴² Cys⁴³ Ser⁴⁴ Val⁴⁵ Cys⁴⁶ Cys⁴⁷

Tyr Ile Thr Leu Ile Ala Ile Leu Ala Ile Leu Asn Pro Leu The
 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55

Gly Pro Glu Ile Lys Asp Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp
 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150

23

〈210〉 27

2222-2233

卷之三

4223 • J. Neurosci., September 2, 2009 • 29(36):4222–4233

5220

232.1 - 232.3

622.2 (123), 6 (1021)

400 27

agtatggagg caacgggtage ccagtgttgc ggggttcataat ttatggaaatggg 60

stratigraphic sequence of geological units 100-120

GGG ATG GCG TTG CCG GTG GCG GCG TGG TCG TCG GCG ATT CGC 169
 Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg
 1 5 10 15

ggc gac gtc tgg gct ccc ggg aac ggg ccc ggg aat and Gln Cys Cys His 217
 Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys
 20 25 30

Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu
 45 46 47

and the other with the other side of the mouth. The mouth is closed and the head is held high. The Ama have very tall, thin, slender, hairless bodies.

Gly Ile Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Thr Ala Arg

Chia Ang Der Alia Leu City Sot Alia Leu Asp Iro Leu Alia Ang Lys Ilo
160 161 162 163 164

gtt cca ctc att tcc atg atc att tcg aga gat mta atg ttt att gtt Val Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala

gct gtt ttt tat atc aua tac cca act ctt cca aua aua ctt aca ctt 793
Ala Val Ile Tyr Val Arg Tyr Arg Thr Leu Pro Thr Pro Arg Thr Ileu
210 215 220

gca aag tat ttc aat ctt tgc tat gca act gct agg tta aad cca aca 841
 Ala Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Ile Lys Pro Thr
 225 230 235

Ter 169 Pro 170 Ser 171 Asp 172 Asn 173 Tyr 174 Asp 175 Ser 176 Ala 177 Val 178 Asn 179 Tyr 180 Asp 181 Ser 182 Ile 183 Tyr 184 Ile 185 Glu

After the first meeting, the first and second authors and the third author (not present at the meeting) discussed the results and the manuscript.

1970-1971
1971-1972
1972-1973
1973-1974

THE BOSTONIAN

Ala; Ala; Trp; Ala; Pro; Gly; Thr; Asp; Pro; Ser; Lys; Arg; Arg; Ala; Cys; Trp

Ala Lys Ile Ile Pro Val Pro Asp Tyr Leu Ile Cys Ileu Ala Glu Arg
45 46 47 48

Trp Arg Ile Lys Arg Pro Ala Ala Ile Ser Gly Ileu Arg Ileu Ileu Ser Gly Ileu Gly

Qln Asp Asn His Cys Ser Gly Ala Gly Iys Ala Ala Pro Arg Pro Ala
65 70 75 80

Ala Gly Ala Gly Ala Ala Ala Thr Ala Pro Gly Gly Glu Thr Gly Pro

Ala Ser Thr Pro Ser Ile Tyr Glu Asn Pro Trp Thr Ile Pro Asn Met
 113 106 113

Ile Ser Met Thr Arg; Ile Gly Leu Ala Pro Val Leu Gly Tyr Ile Ile
115 120 125

Ile-Glu-Glu-Asp-Pro-Asn Ile-Ala-Lys-Gly-Val Phe-Ala-Lys-Ala-Gly
186 187 188 189

Leu Thr Asp Leu Leu Asp Glu Phe Ile Ala Arg Asn Thr Ala Asn Thr
145 150 155 160 165 170 175 180

Arg Ser Ala Ileu Gly Ser Ala Ileu Asp Pro Ileu Ala Asp Ileu Ileu
167 168 169 170 171 172 173 174 175 176 177 178

Wall-E Eye Wall Area: $10\pi \text{ km}^2$ (approx. 314 km^2)

Leu-Tyr-Cys-Lys-Lys-Ala-Lys-Lys-Lys-Lys-Ala-Ala-Ala-Lys-Lys-Tyr-Lys-Tyr

Tyr His Tyr Val Asp Lys Thr Val Glu Val Thr Lys Asp

$$= \frac{1}{2} \frac{\partial^2 \Omega}{\partial x^2} + \frac{1}{2} \frac{\partial^2 \Omega}{\partial y^2} + \frac{1}{2} \frac{\partial^2 \Omega}{\partial z^2}$$

Asp Ala Tyr Pro Lys Thr Leu Glu Asp Ile Arg Val Lys Thr Cys Gly
15 20 25

ggc ggc aac tgg aac ttt gtc aat tgg tt ttc ttc aat tgg ttt ttt ttt ttt
 Gly Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Leu Phe
 36 35 40

ctg tcc gai ctc gag tat tac ctc aca acc gag atg cat cct gag atc 145
 Leu Ser Glu Ileu Gln Tyr Tyr Ileu Thr Thr Glu Val His Pro Glu Ileu
 15 50 55

Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val
b. c. d. e.

CTI IAI CIP SAC AGL RII TPI IIS IAI HII AII AII GAI GII AII AII
Leu Phe Ile His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp
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T₁₀₁₈ T₁₀₁₉ T₁₀₂₀ T₁₀₂₁ T₁₀₂₂ T₁₀₂₃ T₁₀₂₄ T₁₀₂₅ T₁₀₂₆ T₁₀₂₇ T₁₀₂₈ T₁₀₂₉ T₁₀₃₀ T₁₀₃₁ T₁₀₃₂ T₁₀₃₃ T₁₀₃₄ T₁₀₃₅ T₁₀₃₆ T₁₀₃₇ T₁₀₃₈ T₁₀₃₉ T₁₀₄₀ T₁₀₄₁ T₁₀₄₂ T₁₀₄₃ T₁₀₄₄ T₁₀₄₅ T₁₀₄₆ T₁₀₄₇ T₁₀₄₈ T₁₀₄₉ T₁₀₅₀ T₁₀₅₁ T₁₀₅₂ T₁₀₅₃ T₁₀₅₄ T₁₀₅₅ T₁₀₅₆ T₁₀₅₇ T₁₀₅₈ T₁₀₅₉ T₁₀₆₀ T₁₀₆₁ T₁₀₆₂ T₁₀₆₃ T₁₀₆₄ T₁₀₆₅ T₁₀₆₆ T₁₀₆₇ T₁₀₆₈ T₁₀₆₉ T₁₀₇₀ T₁₀₇₁ T₁₀₇₂ T₁₀₇₃ T₁₀₇₄ T₁₀₇₅ T₁₀₇₆ T₁₀₇₇ T₁₀₇₈ T₁₀₇₉ T₁₀₈₀ T₁₀₈₁ T₁₀₈₂ T₁₀₈₃ T₁₀₈₄ T₁₀₈₅ T₁₀₈₆ T₁₀₈₇ T₁₀₈₈ T₁₀₈₉ T₁₀₉₀ T₁₀₉₁ T₁₀₉₂ T₁₀₉₃ T₁₀₉₄ T₁₀₉₅ T₁₀₉₆ T₁₀₉₇ T₁₀₉₈ T₁₀₉₉ T₁₁₀₀ T₁₁₀₁ T₁₁₀₂ T₁₁₀₃ T₁₁₀₄ T₁₁₀₅ T₁₁₀₆ T₁₁₀₇ T₁₁₀₈ T₁₁₀₉ T₁₁₁₀ T₁₁₁₁ T₁₁₁₂ T₁₁₁₃ T₁₁₁₄ T₁₁₁₅ T₁₁₁₆ T₁₁₁₇ T₁₁₁₈ T₁₁₁₉ T₁₁₂₀ T₁₁₂₁ T₁₁₂₂ T₁₁₂₃ T₁₁₂₄ T₁₁₂₅ T₁₁₂₆ T₁₁₂₇ T₁₁₂₈ T₁₁₂₉ T₁₁₃₀ T₁₁₃₁ T₁₁₃₂ T₁₁₃₃ T₁₁₃₄ T₁₁₃₅ T₁₁₃₆ T₁₁₃₇ T₁₁₃₈ T₁₁₃₉ T₁₁₄₀ T₁₁₄₁ T₁₁₄₂ T₁₁₄₃ T₁₁₄₄ T₁₁₄₅ T₁₁₄₆ T₁₁₄₇ T₁₁₄₈ T₁₁₄₉ T₁₁₅₀ T₁₁₅₁ T₁₁₅₂ T₁₁₅₃ T₁₁₅₄ T₁₁₅₅ T₁₁₅₆ T₁₁₅₇ T₁₁₅₈ T₁₁₅₉ T₁₁₆₀ T₁₁₆₁ T₁₁₆₂ T₁₁₆₃ T₁₁₆₄ T₁₁₆₅ T₁₁₆₆ T₁₁₆₇ T₁₁₆₈ T₁₁₆₉ T₁₁₇₀ T₁₁₇₁ T₁₁₇₂ T₁₁₇₃ T₁₁₇₄ T₁₁₇₅ T₁₁₇₆ T₁₁₇₇ T₁₁₇₈ T₁₁₇₉ T₁₁₈₀ T₁₁₈₁ T₁₁₈₂ T₁₁₈₃ T₁₁₈₄ T₁₁₈₅ T₁₁₈₆ T₁₁₈₇ T₁₁₈₈ T₁₁₈₉ T₁₁₉₀ T₁₁₉₁ T₁₁₉₂ T₁₁₉₃ T₁₁₉₄ T₁₁₉₅ T₁₁₉₆ T₁₁₉₇ T₁₁₉₈ T₁₁₉₉ T₁₂₀₀ T₁₂₀₁ T₁₂₀₂ T₁₂₀₃ T₁₂₀₄ T₁₂₀₅ T₁₂₀₆ T₁₂₀₇ T₁₂₀₈ T₁₂₀₉ T₁₂₁₀ T₁₂₁₁ T₁₂₁₂ T₁₂₁₃ T₁₂₁₄ T₁₂₁₅ T₁₂₁₆ T₁₂₁₇ T₁₂₁₈ T₁₂

Am. Ind. Engg. Res. J., Vol. 10, No. 1, March 2018, pp. 1-10. © 2018, IGI Global. This article is based on work supported by grants from the National Science Foundation under Grant No. 1438216. The views and opinions of the authors do not necessarily reflect those of the National Science Foundation.

City of Toledo, Ohio, and the Toledo City Council, Toledo, Ohio, and the Toledo City City Libs Thru Ihr
32

1970-1971. The second edition of the *Handbook of the National Parks* was published in 1973.

Met ¹ Ala ² Ileu ³ Gly ⁴ Ilys ⁵ Ileu ⁶ Ilys ⁷ Glu ⁸ Ilys ⁹ Asp ¹⁰ Ala ¹¹ Tyr ¹² Ilys ¹³ Thr ¹⁴

Ileu Glu Asp Phe Arg Val Ilys Thr Cys Gly Gly Ala Thr Val Thr Ile

Tyr Ile Thr Thr Glu Val His Pro Glu Ile Tyr Val Asp Lys Ser Arg
50 55 60

Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Ile Pro His Met Pro
65 70 75 80

Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln
 85 90 95

Leu Asp Val Glu His Asn Leu Phe Lys Glu Arg Leu Asp Lys Asp Gly
100 105 110

Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu
 115 120 125

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro Asp Arg Cys Glu Ser
130 135 140

Asn Met Thr His Tyr Ile Glu His Leu Ser Ile Gly Glu Asp Tyr Ile
117 282 352

My love for you is like the love that the Ashanti had for Ali. I am a

Ser Met Met Pro Glu Tyr Pro Val Ilys Val Val Iys Pro Val Tyr Met

Lys Val Asp Ile Glu Val Ile1 Arg1 Thr Asn Glu Ile2 Ser Val Thr Arg1
 230 340 350

His Gl. Lys. Wil. Alz. Ash. Fly. Dex. Dex. City. Aug. Fin. Fly. Dex. Bro. Fly.
388 318 319 317 316

lys his Am's and other prop'r his the pen the city val Cns Alabam 11

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His

<210> 31
<211> RNA
<212> DNA
<213> Human MHC class II

5217
5218
5219

44232-30

From the University of California, Berkeley, Calif., the author, Eric L. Lewis, Typ.

11. *What is the primary purpose of the following statement?*

• 1

10

17

1

He Will Stand And See The Appalling Disaster And The Great And Utter Desolation That Shall Cover The Earth And Cover His Eyes The Third Day All Men Shall

any such bill had been introduced by the Chairman of the Committee on Finance.

... and Val Ile Gga Arg Ala Ile Asn Thr Ser Gly Ser Tyr Ala Asn Val Ile Asn
Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met
145 150 155

His Ala Ser Pro Thr Ileu Leu Leu Thr Val Leu Val Ala Leu Thr
160 165 170

Arg Lys Ala Ser Gly Ser His Lys Arg Ser
 140 141

It is a good idea to keep a log of your observations, including a sketch of the site, the date, the time, the weather, and any other relevant information. This will help you to remember what you saw and to compare your observations with those of other naturalists.

1970-1971
1971-1972
1972-1973

Ala Arg Trp Ala His Lys Thr Arg Lys Ile Ser Arg Ala Ile Gly Ser	43	45
Ile Tyr Ile Ala Tyr Tyr Ser Ile Ile Val Thr Ile Ile Ile Ile Asp	47	49
Ile Ile Arg Ser His Cys Ile Thr Ile Ala Met Ile Ser Ile Pro Arg	51	53
Met Ile Ser Ile Asp Thr Pro Ala Ala Tyr Ser Ile Gly Ile Ala Ile	55	57
Ile Gly Ile Ile Val Val Leu Val Ile Ser Ser Ile Ile Ala Ile Gly	59	61
Phe Ala Gly Thr Phe Ile Gly Asp Tyr Ile Gly Ile Leu Lys Glu Ala	65	67
115	117	120
Arg Val Thr Val Phe Pro Phe Asn Ile Ile Asp Asn Pro Met Tyr Trp	130	132
130	132	140
Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Ile Met His Ala Ser Pro	145	147
145	147	150
Thr Gly Ile Ser Ile Ile Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala	165	167
165	167	170
Ile Leu Tyr Ile Gly Pro Phe Thr Ala Gly Ile Tyr Arg Ile Lys Ala	180	182
180	182	185
Ser Gly Ser His Lys Arg Ser	185	

<210> 33
<211> 901
<212> DNA
<213> *Homo sapiens*

For more information, contact the Office of the Vice President for Research and the Office of the Vice President for Student Affairs at 319-335-1111, or visit www.iowa.edu.

Arg Thr Pro Val Ile Ile Asp Glu Glu Lys Lys Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Ileu Met Leu His Ala
51 52 53 54 55 56 57 58 59 60 61 62 63 64

Asn Gly Ser Ileu Glu Asp Pro Ile Asn Pro His Glu Ala His Thr

am gtr atc atā gad dīg val ille ala val dīd add gyt gad dīg dī
Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala
96 100 104 110

Asn Asp Cys Arg Gln Thr Asp Val Asp Asn Asp Asp Asn Thr Phe Arg Gly Phe Thr Asn Ile Gln Thr Leu Ile Leu Pro Gln
115 120 125

rat gtc aac tgt cat ggg aat aat gat tgg aat act aat aat aat 434
 His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser
 133 134 135 136 137 138 139 140

tat ata gac aac caa ata tgt gca ggg caa aag aac ott tgc aat aac 451
 Tyr Ile Asp Asn Gln Ile Cys Gln Gly Glu Lys Asn Ile Cys Asn Asn
 115 116 117 118 119 120 121 122 123 124 125 126 127 128

arg ggg gac cca gaa atg ttt ttt ttt ttt gga ttt ttt gtg gtg gat gat 530
 Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp
 162 163 164

ggc cca ggt cit ttc cag tgc gtt ttt ggt gat ggt ttc cat gga taa 578
 Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr
 176 180 184 186 188

aaa ttt atg cgg cag ggt gtt ttt ttt atg ttt ttc ggg att 626
 Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile
 195 200 205

that the first stage of the process is to identify the main features of the system and to determine the most important variables that affect the system's behavior.

• 11.000
• 11.000 IPT
• 11.000 Human proteins

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro Trp Ala
1 5 10 15

Ala Ala Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala Leu Pro
20 25 30

Glu Ile Cys Thr Glu Cys Pro Gly Ser Val Glu Arg Leu Ser Lys Val
35 40 45

Ala Ile Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala Arg Cys
50 55 60

Cys Leu Asn Glu Lys Gly Thr Ile Leu Gly Leu Asp Leu Glu Asn Cys
65 70 75

Ser Leu Glu Asp Pro Gly Pro Asn Ile His Glu Ala His Thr Thr Val
80 85 90

Ile Ile Asp Leu Glu Ala Asn Pro Leu Lys Gly Asp Leu Ala Asn Thr
100 105 110

Phe Arg Gly Phe Thr Glu Leu Glu Thr Leu Ile Leu Pro Glu His Val
115 120 125

Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile
130 135 140

Asp Asn Glu Ile Cys Glu Gly Glu Lys Asn Leu Cys Asn Asn Thr Gly
145 150 155 160

Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp Gly Pro
165 170 175

Gly Leu Leu Glu Cys Val Cys Ala Asp Gly Ile His Gly Tyr Lys Cys
180 185 190

Met Asn Ile Ile Asp Ile Asp Ile Asp Ile Asp Ile Asp Ile Asp
195 200

Ala Thr Ile Leu Asp Val Asp Ile Asp Ile Asp Ile Asp Ile Asp
210 215 220

Lys Ala Lys Thr Ser
225 230

420 JOURNAL OF CLIMATE

May the Lord bless my King.

Leu Lys Leu Leu Thr Thr Val Gly Leu Thr Leu Ile Thr Arg Gly Glu

Arg Thr Ala Gln Asp Arg Thr Asp Thr Ser Ser Ser Ser Ser Ala Asp Ser Thr Ile Met
(b) 27 32

Asp Asn Gln Gln Asp Asp Gln Val Pro Thr Arg Ala Val Tyr Thr Val Leu
10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

ccc gag acc cag acc cag caa ctg gaa gga asp; Met asp ser Ala gln; 236
 Pro Gin Thr Gin Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val
 75 80 85

aca gat cca gag aca cac aag agc aca aca gca gat aca aat gat 344
 Thr Asp Pro Glu Thr His Ser Thr Lys Ala Ala His Pro Thr Asp
 90 95 100

gat acc acg acg ctc tct ga; aja cca ttt cca aat aca gac gtc cag 392
 Asp Thr Thr Thr Leu Ser Glu Arg Ile Ser Pro Ser Thr Asp Val Gln
 105 110 115

ATA GAC TCC TGG ACC CTC AGG GAA TTT GGT TTT CAT GAG GAT GAT GAC 440
 Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro
 120 125 130

and the following fragments obtained from the sequencing gel:
 a) fragment containing peptide 1 (the first 10 amino acids of fragment 1),
 and b) fragment 1.

"41

Peptides:
 1: 1-10
 2: 11-17
 3: 18-27
 4: 28-34

Sequence:
 Met Ser Pro Ser Gly Arg Leu Tyr Leu Leu Thr Ile Val Gly Leu Ile
 1 2 3 4 5 6 7 8 9 10 11 12 13

Leu Pro Thr Arg Gly Gln Thr Leu Lys Arg Thr Thr Ser Ser Ser Ser
 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29

Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 35 36 37 38 39 40 41 42

Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 50 51 52 53 54 55 56 57 58 59 60

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80

Thr Asp Gly Pro Leu Val Thr Asp Pro Gln Thr His Lys Ser Thr Lys
 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

Ala Ala His Pro Thr Asp Asp Thr Thr Leu Ser Glu Arg Pro Ser
 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115

Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly
 116 117 118 119 120 121 122 123

Pro His Thr Asp Asp Pro Pro Pro Tyr Asp Glu His Thr Leu Arg Lys
 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145

Arg Gly Leu Leu Val Ala Val Leu Ile Ile Thr Gly Ile Ile Ile
 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162

Leu Ile
 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179

Arg Arg

Peptides:
 1: 1-10
 2: 11-17
 3: 18-27
 4: 28-34

1. *Leucosia* *leucosia* (L.) *leucosia* (L.) *leucosia* (L.) *leucosia* (L.)

4. - 5. - 6. - 7. - 8.

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President of the Republic of the Philippines and the
Minister of the Philippines

Arg-Tyr-Gly-Ala-Ala-Tyr-His-Val-Phe-Lys-Gly-Ala-Ala-Ala-Arg-Gln-Ala-Arg 212

Arg Gln Asp Ile Gaa Arg Lys Asp Ile Gaa Arg Ile Gaa Arg Asp Gln Arg Arg Asp Gly Arg Asp Glu Gln Ser Thr Ile Glu Ser Gln Glu Trp Asn Pro
55 60 65

Trp Gln Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser
 356

ctt gaa atg ttt gat aaa tcc acc aaa ggt aaa aca gat ctc acf gta 404
Leu Gln Ile Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val
-50 -40 -30 -20 -10

...aa ate tgg iij add act ggc att ggc tgg tat ctc tgg gag cat att 452
Gln Ile Trp Ile Lys Ala Ala Ile Gly Lys Tyr Ile Trp Glu His Ile

Pro-Phe-Lys-Ala-Asn-Gly-Gly-Lys-Val-Glu-Lys-Lys-Phe-Tyr-Tyr

Tyr Asp Ser Pro Thr Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu
230 235 240

345 Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Thr Ser 350 355 360

Met Ile His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile
265 270 275

Tyr Glu Asn Ser Ser Arg Cys Ala Leu Met Asn Ile Leu Lys Lys Asp
280 285 290

ggg aac gat aag ati tgg gct tta gca aca gaa ctc tag cct 1828
 Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu Trp His Trp Gln Pro
 240 300 305

cag gaa aat gat gaa agt ttt aag aat tac caa gat gtt ttt tt ca; 1076
 Gln Glu Ile Asn Glu Ser Ileu Lys Asn Tyr Gln Asp Ala Leu Ileu Glu
 310 315 320

agt gat ttt aca ttt tgc ttt gtc ttt gta aac aca gaa tgc tat cga 1124
 Ser Asp Ileu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg
 325 330 335 340

atc tat gac gtt ttt tcc tat ggc ttt att ctt gtc ttt gaa ttt gtt 1172
 Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val
 345 350 355

Top layer of sand is 100% fine sand and has a thickness of 100'. The layer is followed by a 10' thick layer of fine sand and a 10' thick layer of sand.

the last Met, Asn, Asn, Lys, Ser
44.

Met Arg Leu Thr Arg Lys Arg Ile Cys Ser Ile Leu Ile Ala Leu Tyr
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

Cys Leu Phe Ser Leu Tyr Ala Lys Tyr His Val Ile Thr Gly Ile Ile

Arg-Gln-Ala-Pro-Ala-Gly-Ser-Pro-Arg-Gly-Lys-Arg-Lys-Gly-Ala-Ala

Pro Ala Arg Glu Arg Arg Gly Arg; Glu Gln Ser Thr Leu Val Ser Glu
 50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Glu Gln Glu His Arg
 65 70 75 80 85 90

Phe Lys Thr Ser Ile Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
 85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
106 105 106

Trp Glu His Ile Phe Glu Gly Ser Leu Asp Pro Ser Asp Val Thr Ala
 115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe
 130 131 132 133 134 135 136

227	237	247	248
Ala Trp Pro Leu Ile Val Ala Thr Tyr Arg Asn Ile Pro Val Val Ala			
245	250	251	
Ala Ser Thr Cys Met Leu His Arg Glu Arg Ile Pro Tyr Leu Lys Arg Pro			
260	264	265	
Leu Gly Thr Ile Tyr Glu Asn Ser Arg Ile Ala Leu Met Asn Ile			
270	280	285	
Leu Lys Lys Asp Lys Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Ile			
290	295	300	
His Trp Gln Ile Ile Ala Thr Arg Glu Ser Leu Lys Asn Tyr Gln Asp			
305	310	315	320
Ala Leu Ile Glu Ser Arg Leu Thr Leu Cys Pro Val Gly Val Asn Thr			
325	330	335	
Glu Cys Tyr Arg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val			
340	345	350	
Val Glu Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His			
355	360	365	
His Gly Ala Pro Ile Glu Leu Lys Ser Met Gly Ala Pro Phe Ile			
370	375	380	
Phe Ile Lys Asn Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys			
385	390	395	400
Thr Ile Ile Leu Glu Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln			
405	410	415	
Trp Tyr Gln His Ile Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile			
420	425	430	
Leu Glu Ser Ser Phe Leu Met Asn Asn Lys Ser			
435	440		

227-237
237-247
247-251
251-265
265-270
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965-970
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975-980
980-985
985-990
990-995
995-1000

Arg Pro Val Glu Ala Glu Glu Ala Thr Glu His Arg Leu Lys Pro Thr
115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130

Val Leu Ile Ala Asn Arg Leu Thr Cys Ser Lys Ala Arg Ala Glu Asp
 50 55 60

Arg-Lys-Lys-Lys-Glu-Ala-Lys-Lys-Glu-Glu-Lys
Arg-Lys-Lys-Glu-Ala-Lys-Lys-Glu-Glu-Lys

Arg Arg Arg Arg Asn Arg Asp Glu Arg Lys Lys Lys Lys Thr Ala Lys Glu Glu Glu Ser Asn Leu Lys
135 145 155

ctg gat ctg gag gaa aaa gag ccc gga taa cat taa aag aag aag 443
 Lys Asp Lys Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser
 115 120 125

492
aia gtc atg tgaagatttc tggatgcctc tttagggat tttccggat
Thr Val Met
3.

• 27 • 45

Ile Val Asp Ala Val Glu Ala Phe Val Glu His Arg Ile Lys Ile Thr Ile
 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

Val Glu Ile Ala Ala Val Val Glu Phe Ile Ile Ile Val Tyr Leu Val
 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300

Glu Ile Thr Thr Ile Arg Met Glu Ser Asn Leu Tyr Ile Asp Glu Ser
 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500

Lys Lys Glu Lys Lys Thr Ala Lys Ile Glu Glu Ser Asn Leu Asp Leu
 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600

Asp Leu Ile Glu Lys Glu Ile Glu Asp His Glu Arg Ala Lys Ser Thr
 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700

Val Met
 710

<210> 41
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric
 cDNA-RNA oligonucleotide

<400> 41

GGGGGGTTCCTTGGG

14

<210> 42

<211> 126

<212> PRT

<213> Artificial Sequence

<400> 42

Met Asp Ile Val Leu Ile Asp Glu Ile Asp Glu Asp Asn Asp Asn Asp
 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

Asp Asp His Thr Leu Ile Tyr Ile Asp Lys Ser Asp Ala Asp Ser Asn
 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000

Asp Ala Asp Thr Ile Val Leu Ile Tyr Ile Asp Lys Ser Asp Ala Asp Ser Asn
 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000

10

1

200

1

Arg-Lys-Lys-Ala-Ala-Ser-Val-Tyr-Tyr-Tyr-Asp-Ser-Pro-Lys-Tyr-Ala

Sly Ile Ser Val Ser Phe Val Tyr Val Ile Arg Ala Arg Thr
Ile Ile Ile Ile Ile Ile Ile

521.2 1985
521.2 1985
521.2 1985
521.2 1985

2400 x 43

Met Ser Met Ser Leu Glu Ile Thr Gly Thr Ser Leu Ala Val Ile Gly
 1 5 10 15

Trp Ile Cys Thr Ile Val Cys Cys Ala Ileu Pro Met Trp Arg Val Ser
 20 25 30

Ala Pro Ile Gly Ser Ser Ile Ile Thr Ala Gln Ile Thr Trp Gly
36 40 44

Leu Thr Met Asn Cys Val Gln Ser Thr Gly Glu Met Gln Cys Lys Met
30 35 60

Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala
65 70 75 80

Ile Ile Val Val Ser Ile Ileu Leu Ala Ala Phe Gly Ileu Leu Val Ala
85 90 95

Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Ile Ala Ala Val
112 113 114 115 116 117

Ala Thr Ala Tyr Asp Arg Ilys Thr Thr Ser Glu Arg Pro Gly Ala Arg

Thr Pro His His His His Tyr Glu Ile Met Ser Tyr Pro Thr
125 130 135 140 145 150 155 160 165 170 175 180 185

211-44
211-96
212-187
213-*Caenorhabditis elegans*

Leu Val Ser Val Ser Ala Phe Thr Ala Ile Ile Gly Ile Gly Gly Ile

Trp Ile Val Pro Lys Gly Pro Asn Arg Gly Ile Ile Gln Leu Met Ile
 35 40 45

Ile Met Thr Ala Val Cys Cys Trp Met Ile The Trp Ile Met Val The Leu
50 55 60 65 70 75 80 85 90

His Gin Ieu Asn Pro Leu Ile Gly Pro Cln Ile Asn Val Lys Thr Ile
65 70 75 80

Arg Trp Ile Ser Glu Lys Trp Gly Asp Ala Pro Asn Val Ile Asn Asn
50 90 95

- 210 - 45
- 211 - 246
- 212 - FRT
- 213 - *Caenorhabditis elegans*

Met Ile Val Thr Ser Met Phe Arg Gly Ile Ala Cys Arg Cys Glu Leu
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

110	111	112
Ser Val Leu Asp Pro Val Ala Asp Lys Leu Leu Ile Ser Thr Met Pro		
113	114	115
Ala Thr Met Thr Tyr Ala Gly Leu Ile Pro Leu Pro Leu Thr Ser Val	116	117
Val Ile Leu Arg Asp Ile Cys Leu Ile Gly Gly Gly Ile Tyr Lys Arg	118	119
Tyr Gln Val Met Ser Pro Pro Tyr Ser Leu Ser Arg Ile Phe Asp Pro	120	121
Gln Val Ser Ser Met Gln Val Val Pro Thr Met Met Ser Lys Ile Arg	122	123
Thr Val Leu Gln Ile Thr Leu Val Ala Leu Ser Leu Ser Ser Pro Val	124	125
Ile Asp Ile Ser Thr Gly Ala Asn Asp Val Ile Val Gly Leu Gly Cys	126	127
Ile Thr Gly Ile Thr Thr Ile Tyr Ser Gly Leu Gln Tyr Ala Ser Gly	128	129
Lys Ala Ile Lys Lys Ile	130	
	245	
+210-46		
+211-462		
+212-3RT		
+213- Ctenorhabditis elegans		
+230-46		
Met Ser Leu Leu Trp Ser Leu Lys His Phe Asp Ala Tyr Arg Lys Pro	1	10
	9	11
Met Asp Asp Phe Arg Val Lys Thr Leu Ser Gly Gly Ile Val Thr Leu	11	20
	20	30
Ile Asp Ile Ile Asp Ile Val Ile Ile Ile Val Ile Ile Ile Ile Ile Ile	30	40
Ile	40	50
Asp Asp Ala Arg Val His Ile Ile Ile Asp Ile Thr Ile Thr Thr Lys Leu	50	60
	60	70
Ile	70	80

Gly Arg Asn Ile Ser Gln Ser Ala Gln Lys Ile Val Ile Asn Ala Asn
 111 112 113
 Lys Thr Ser Val Gln Thr Thr Asp Val Ile Gln Val Val Lys Cys Gly
 114 115 116 117
 Ser Cys Tyr Ily Ala Ala Ala Asp Gly Ile Cys Tyr Asn Thr Cys Asp
 118 119 120 121 122 123
 Asp Val Lys Ser Ala Tyr Ala Val Lys Ily Thr Gln Val Asn Ile Ile
 124 125 126 127 128 129
 Gln Val Gln Gln Cys Lys Asn Asp Lys Thr Val Lys Gln Ile Asn Gln
 130 131 132 133 134 135
 His Lys Asn Glu Gly Cys Arg Val Tyr Ily Thr Val Lys Val Ala Lys
 136 137 138 139 140 141
 Val Ala Gln Asn Phe His Leu Ala Phe Ily Asp Pro His Gln Ala Met
 142 143 144 145 146 147
 Arg Ser His Val His Asp Leu His Asn Leu Asp Pro Val Lys Phe Asp
 148 149 150 151 152 153
 Ala Ser His Thr Val Asn His Val Ser Ile Gly Lys Ser Phe Pro Gly
 154 155 156 157 158 159
 Lys Asn Tyr Pro Leu Asp Gly Lys Val Asn Thr Asp Asn Arg Gly Gly
 160 161 162 163 164 165
 Ile Met Tyr Gln Tyr Tyr Val Lys Val Val Pro Thr Arg Tyr Asp Tyr
 166 167 168 169 170 171
 Leu Asp Gly Arg Val Asp Gln Ser His Gln Phe Ser Val Thr Thr His
 172 173 174 175 176 177
 Lys Lys Isp Leu Gly Phe Arg Gln Ser Ily Leu Pro Gly Ile Phe Ile
 178 179 180 181 182 183
 Gln Tyr Gln Ile Ser Pro Leu Met Val Gln Tyr Gln Glu Phe Arg Gln
 184 185 186 187 188 189
 Ser Ile Asn Asp Pro Leu Val Asp Leu Ile Asp Asp Ile Val Ile Asp
 190 191 192 193 194 195
 Ile Ala Val Asp Ile Ile Val Asp Ile Ile Val Ile Val Ile Val Ile
 196 197 198 199 200 201
 Tyr Met Lys Ser Arg Ile Ala Ily Gly Ile Lys Thr

Arg	Leu	Leu	Leu	Thr	Val	Leu	Gly	Tyr	Val	Asp	Pro	Ser	Thr	Gln	Pro	Ser	Val	Ala
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Ala	Val	Leu	Thr	Ile	Val	Thr	Asn	Pro	Leu	Pro	Trp	Asn	Val	Val	Ala			
Asp	Trp	Val	Gln	Arg	Thr	Arg	Ile	Leu	Pro	Asp	Ala	Pro	Ile	Val	Pro	Asp	Val	Ala
19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1
Tyr	Ile	Ala	Cys	Tyr	Asp	Leu	Ile	Ser	Ile	Ile	Leu	Leu	Asn	Ile				
19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1
Leu	Arg	Pro	His	Cys	Phe	Thr	Gln	Ala	Met	Met	Ser	Gln	Pro	Lys	Met			
6	5	4	3	2	1													
Ile	Gly	Leu	Asp	Ser	His	Thr	Ile	Tyr	Phe	Ile	Ile	Ile	Ala	Leu	Leu			
85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103
Ile	Tyr	Gly	Leu	Val	Phe	Val	Ile	Ser	Leu	Pro	Tyr	Ala	Leu	Gly	Phe			
100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118
Thr	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly	Ile	Ile	Ile	Lys	Ile	Ser	Arg		
115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133
Val	Thr	Thr	Phe	Pro	Phe	Ser	Val	Leu	Asp	Asn	Pro	Met	Tyr	Trp	Gly			
130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148
Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Leu	Met	His	Ala	Ser	Pro	Thr			
145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163
Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu	Val	Tyr	Val	Val	Ala	Leu			
165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183
Leu	Phe	Glu	Gln	Pro	Phe	Thr	Ala	Gly	Ile	Tyr	Arg	Arg	Lys	Ala	Thr			
180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198
Arg	Ile	His	Lys	Arg	Arg	Ser												
198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216

111 Ala Thr Gly Ser Ile Thr Ala Ala Gln Thr Ala Thr Ile Leu
112 113 114 115 116 117 118 119 120 121 122

Leu Lys Met Ala Thr Ile Arg Pro Val Ser Asp Pro Gly Ile His Thr
123 124 125 126 127 128 129 130 131 132

Pro Ser Lys Lys Gly Thr Ile Ala Val Ser Arg Ile Glu Pro Leu Ser
133 134 135 136 137 138 139 140 141 142

Pro Ser Lys Asp Pro Met Pro Ser Tyr Ile Ala His Ile Leu Asp
143 144 145 146 147 148 149 150 151 152

Pro Asn Glu Asn Asn Pro Ile Tyr Tyr Asp Asp Thr Ile Leu Arg Lys
153 154 155 156 157 158 159 160 161 162

Asp Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Ile Ile Ile Ile
163 164 165 166 167 168 169 170 171 172 173 174 175

Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Gln Phe Cys Leu Asn Arg
176 177 178 179 180 181 182 183 184 185 186 187

His Arg